

# IEDB Analysis Resource

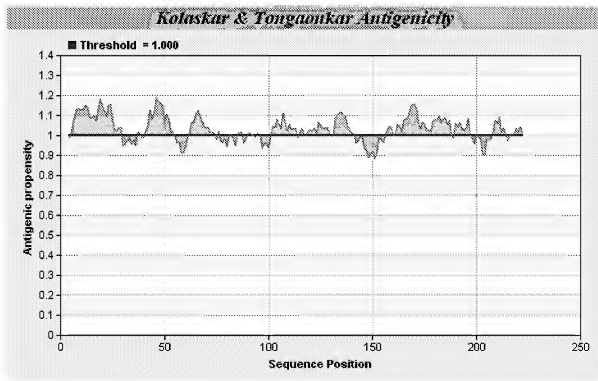
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## Kolaskar & Tongaonkar Antigenicity

### Sequence:

1 MIFFKPSTVV LTASALALSG CVADPVTGQQ SPNKSAMYGL GGAAVCGIVG ALTHSGKGAR  
 61 NSALACGAIG AGVGGYMDIQ EQRLRQNLG TQIEIQRQGN QIRLVMPESV TFAIGSAALG  
 121 GSAQYALNTA AQTIVQYFDT TLTINGHTDN TGSDAVNNPL SQHRAQAVAY YLQTRGVAAS  
 181 RLFVYGYGSH MFVASNATVE GRAQNRRLVEI LINPDQRAVN AARHM

Center position: 4 Window size: 7



Average: 1.032 Minimum: 0.887 Maximum: 1.190 Threshold: 1.000

[Click here to view plotted values in table format](#)

### Predicted peptides:

No.	Start Position	End Position	Peptide	Peptide Length
1	5	29	KPSTVLTASALALSGCVADPVTGQ	25
2	41	54	GGAAVCGIVGALTH	14

3	62	74	SALACGAIGAGVG	13
4	102	113	IRLVMPESVTFA	12
5	115	129	GSAALGGSQAQYALNT	15
6	132	141	QTLVQYPDTT	10
7	161	188	SQHRAQAVAYYLQTRGVAASRLTVYGYG	28
8	190	197	HMPVASNA	8
9	208	213	VEILIN	6

**Reference:** [Kolaskar AS, Tongaonkar PC. A semi-empirical method for prediction of antigenic determinants on protein antigens. FEBS Lett. 1990 Dec 10;276\(1-2\):172-4.](#)

**Scale values:** A:1.064, C:1.412, D:0.866, E:0.851, F:1.091, G:0.874, H:1.105, I:1.152, K:0.93, L:1.25, M:0.826, N:0.776, P:1.064, Q:1.015, R:0.873, S:1.012, T:0.909, V:1.383, W:0.893, Y:1.161